

FIG. 1A

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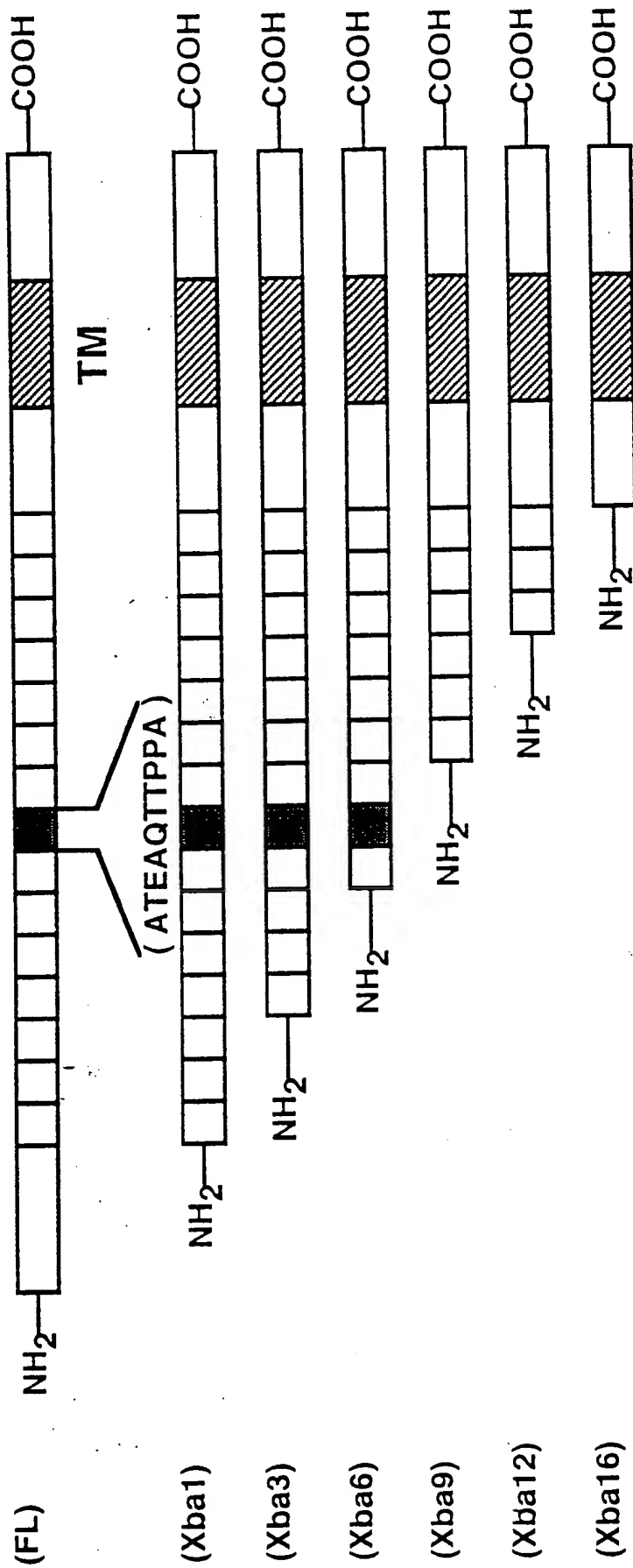


FIG. 1B

P-Selectin Binding to COS M6 Cells
Expressing PSGL-1-NH2 Gross Deletion
Mutants

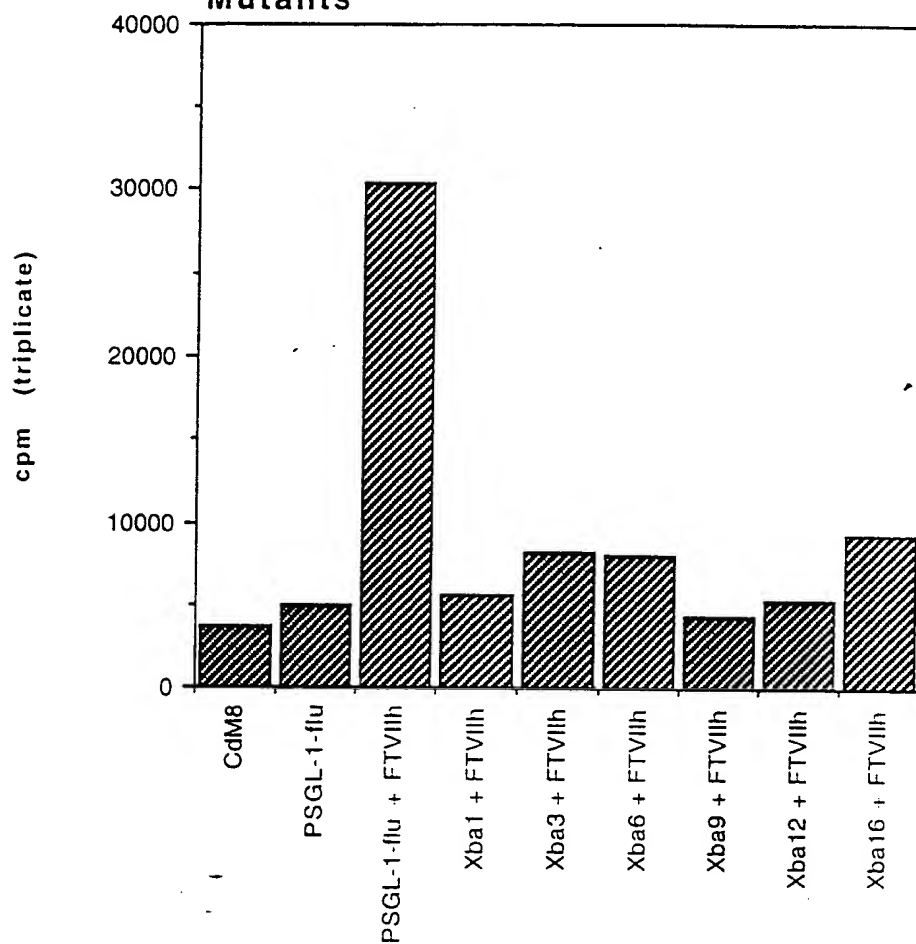


FIG. 2A

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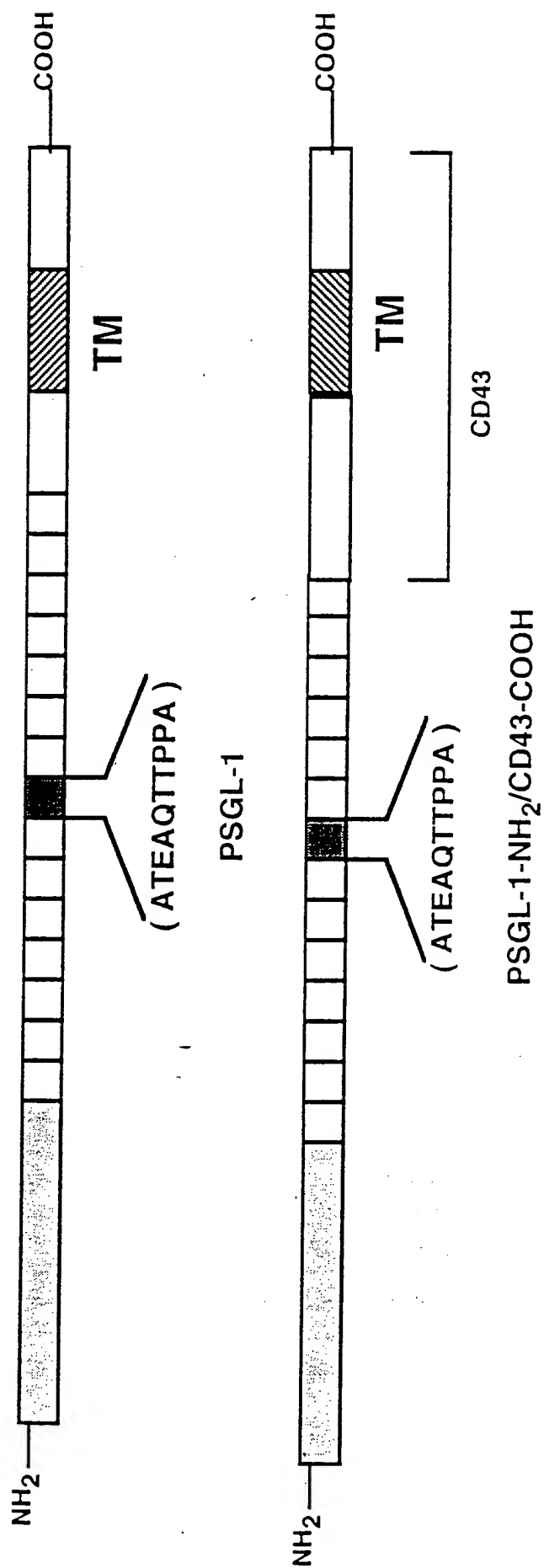


FIG. 2B

P-Selectin Binding to COS Cells Expressing
Chimeric PSGL-1/CD43 Constructs

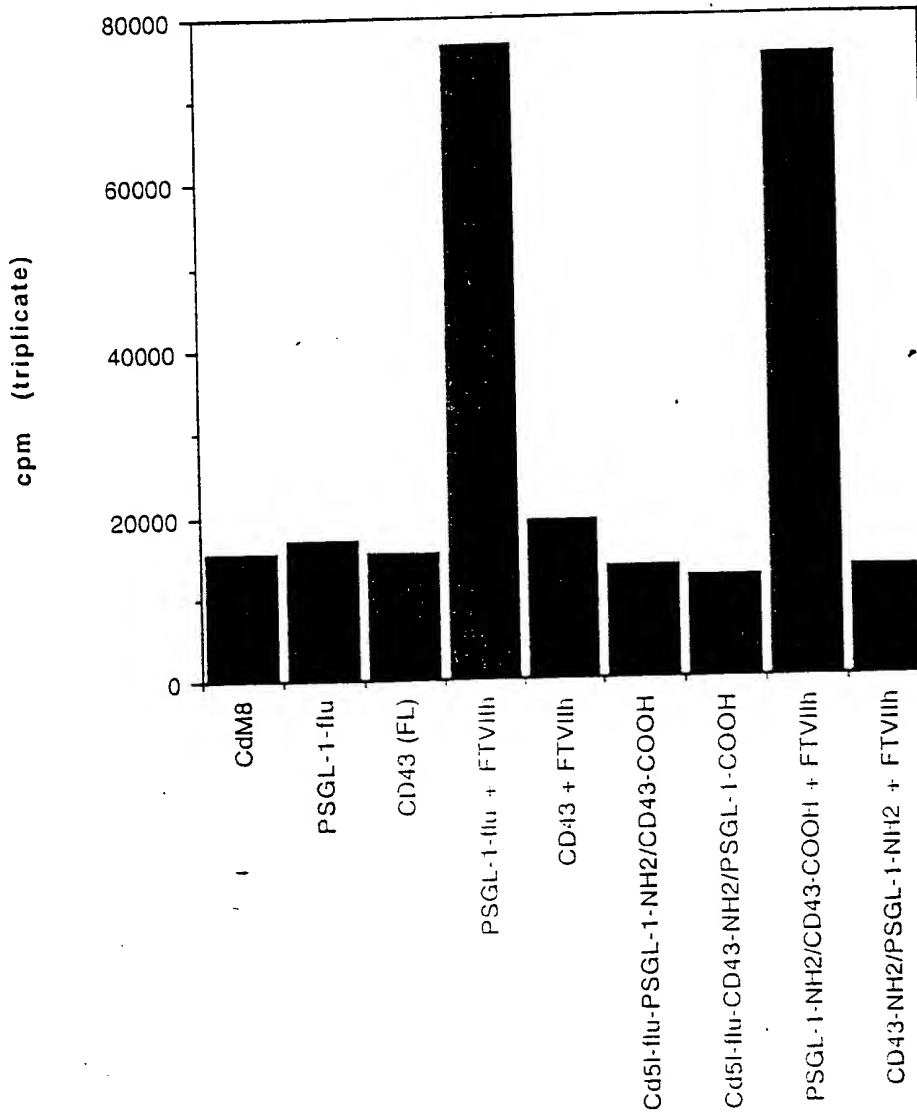


FIG. 3A

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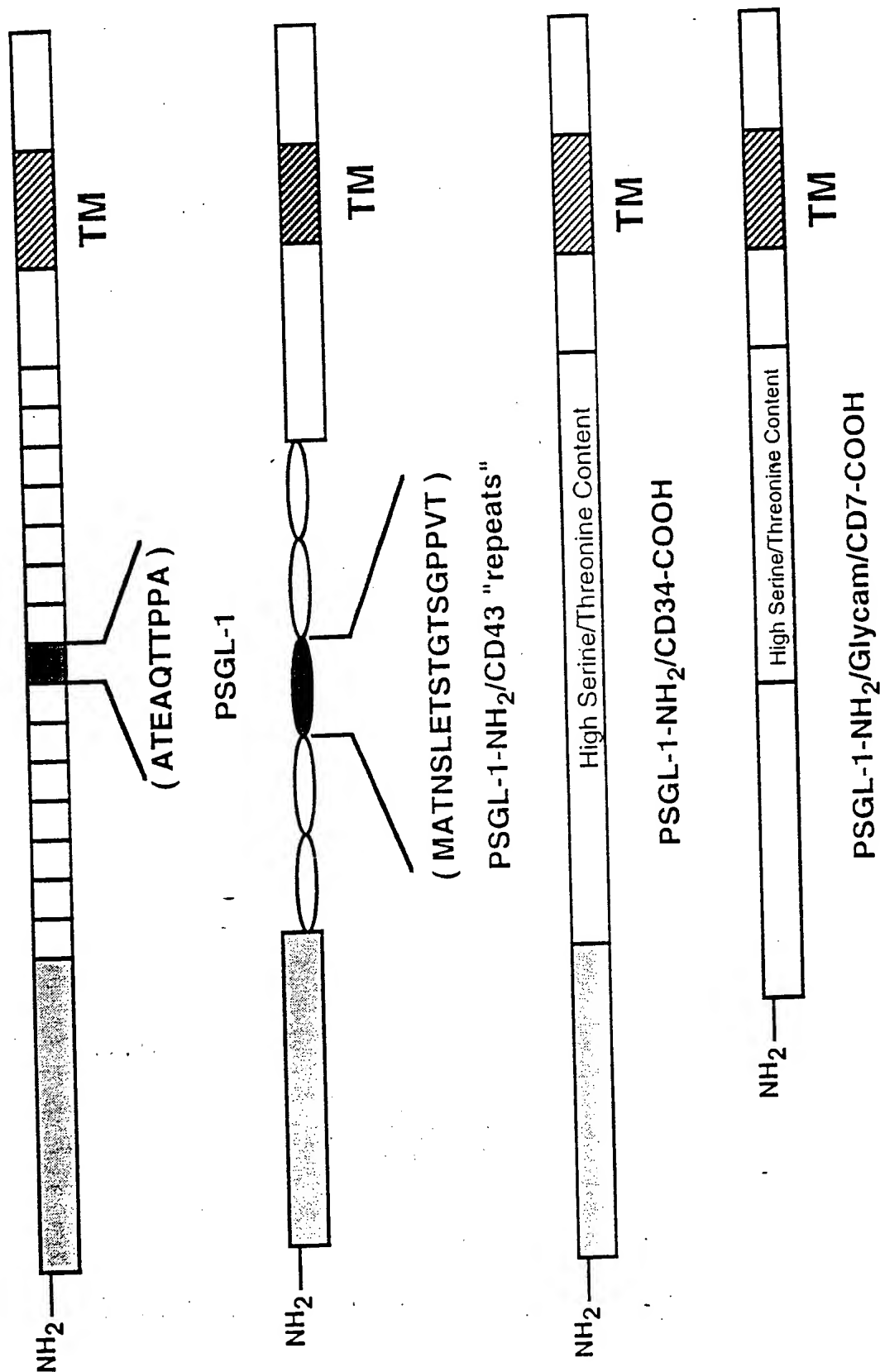


FIG. 3B

P-Selectin Binding to COS M6 Cells
Expressing PSGL-1-NH2/Mucin Chimeric
Constructs

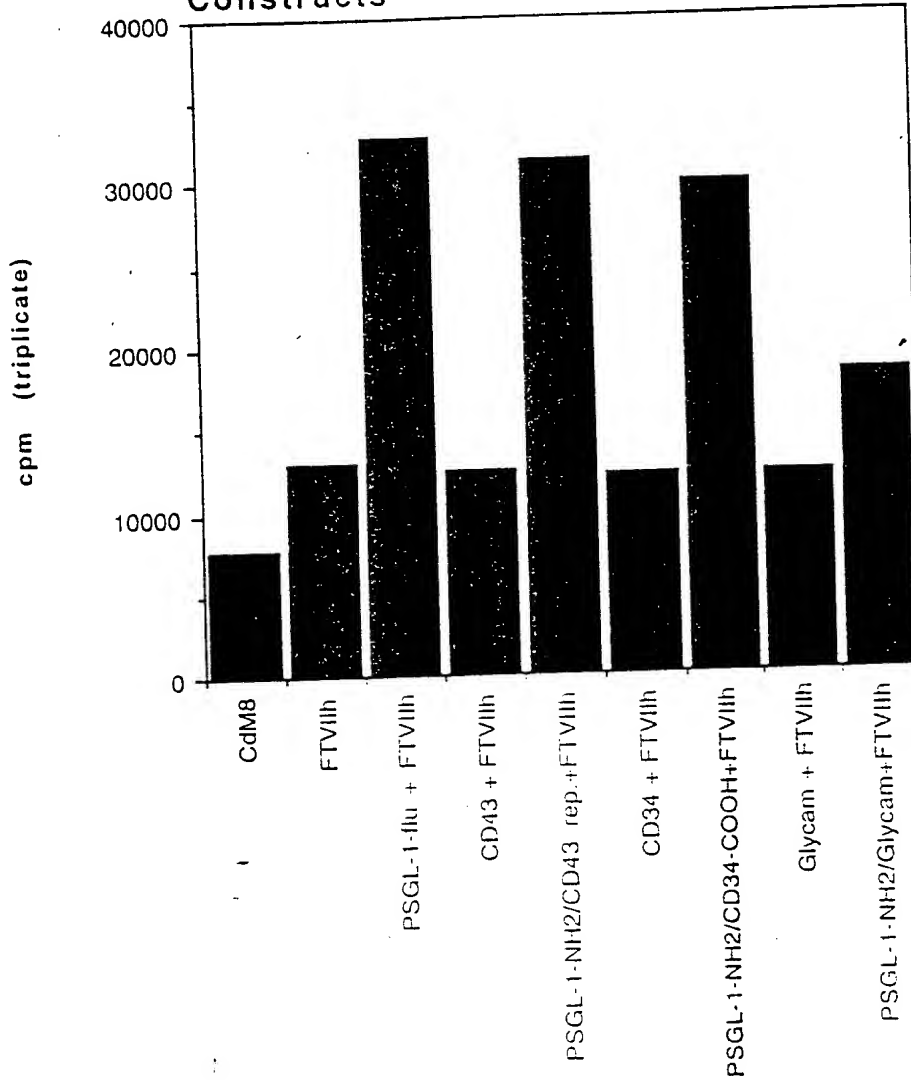
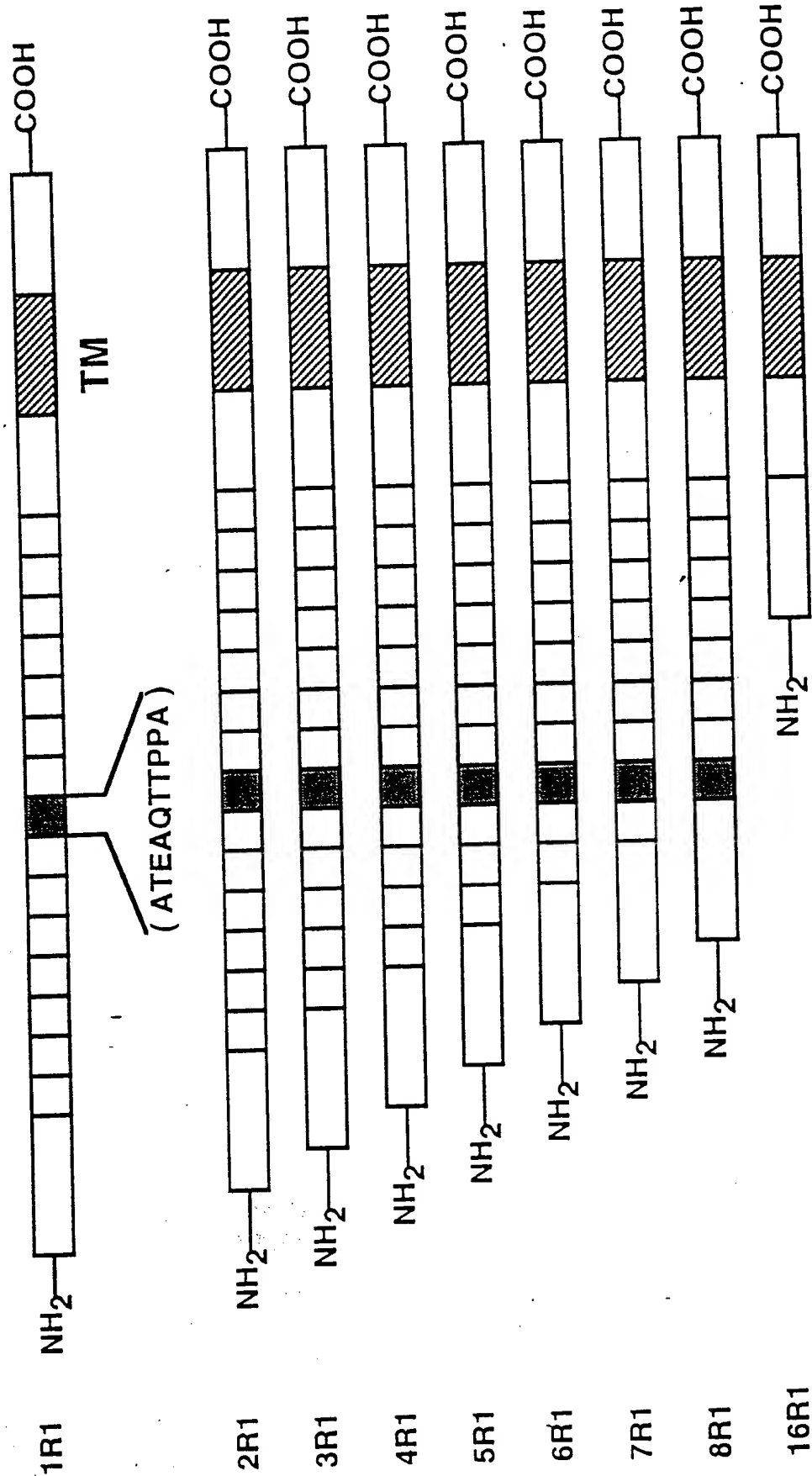


FIG. 4A

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FIG. 4B

P-Selectin Binding to COS M6 Cells
Expressing PSGL-1 Internal Deletion
Mutants

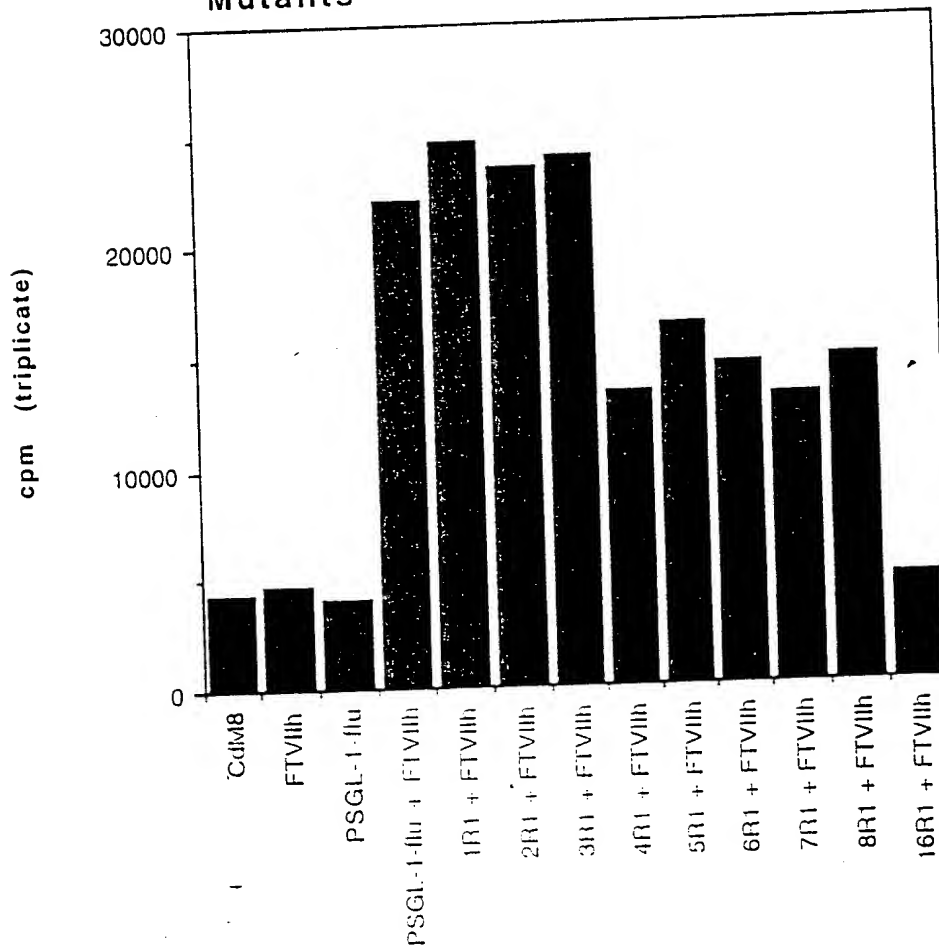


FIG. 5

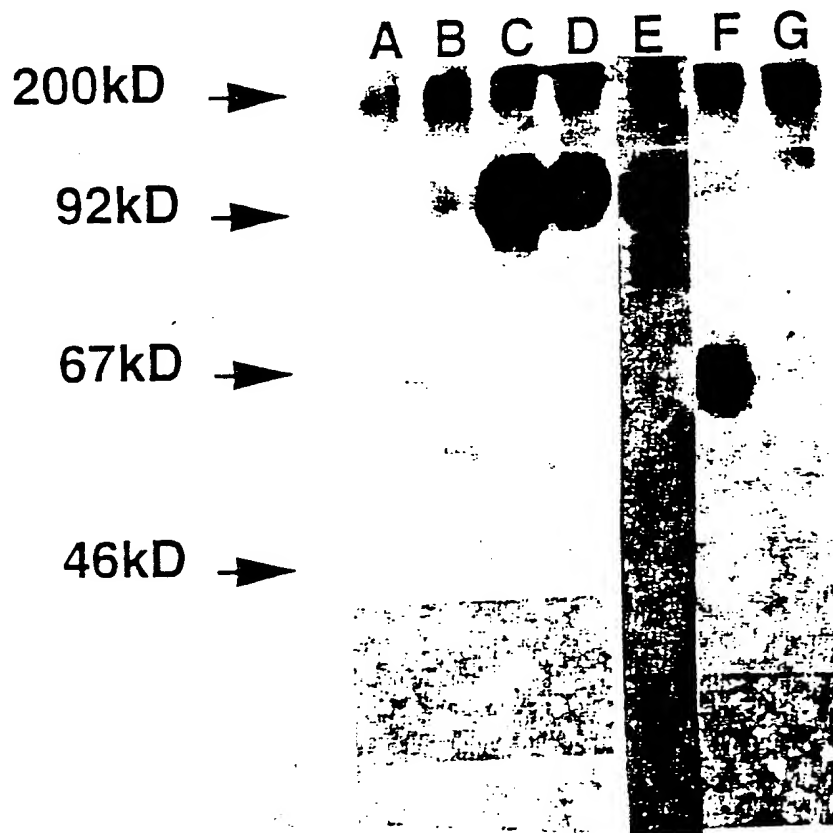
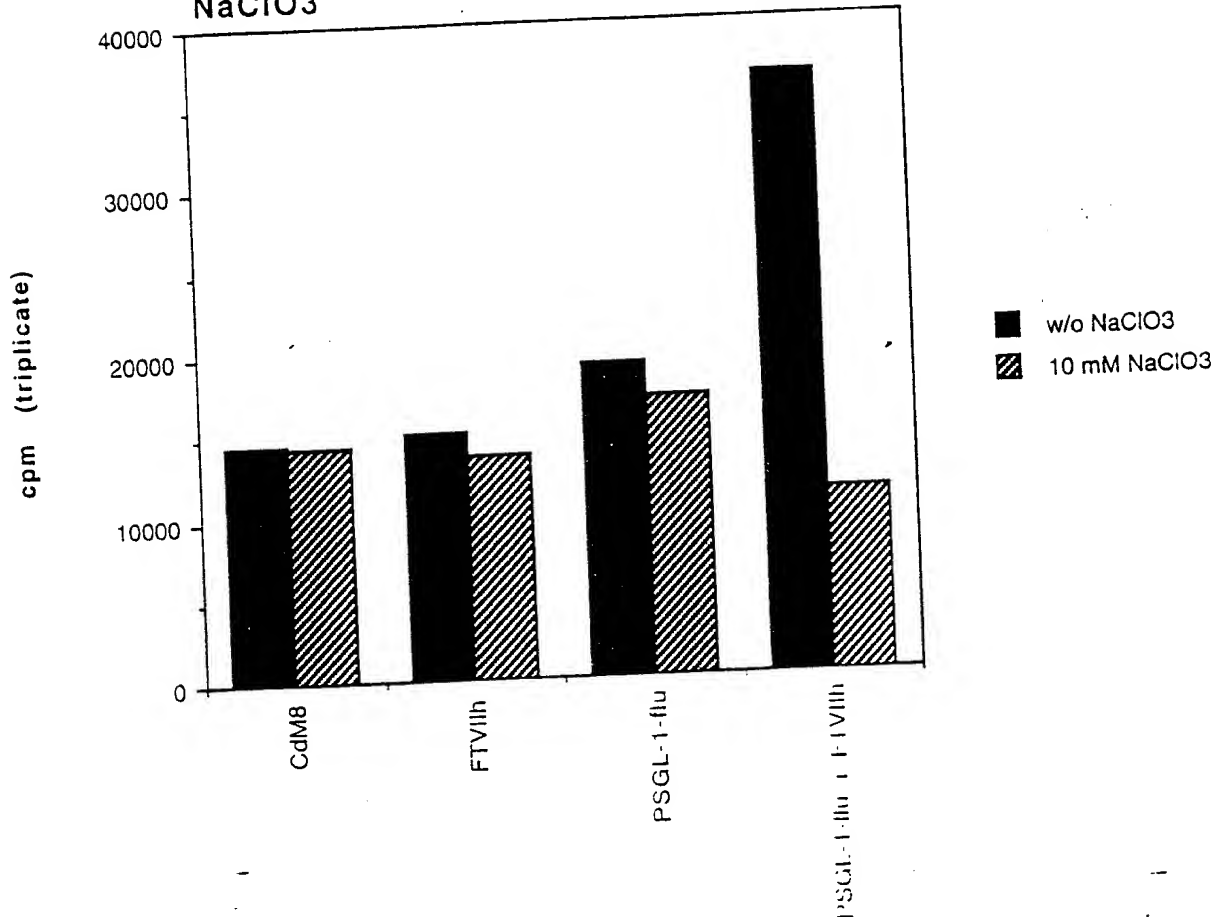


FIG. 6A

P-Selectin Binding to COS M6 Cells
Expressing PSGL-1/FTVIIh w and w/o
NaClO₃



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FIG. 6B

E-Selectin Binding to COS M6 Cells
Expressing PSGL-1/FTVIlh w and w/o
NaClO₃

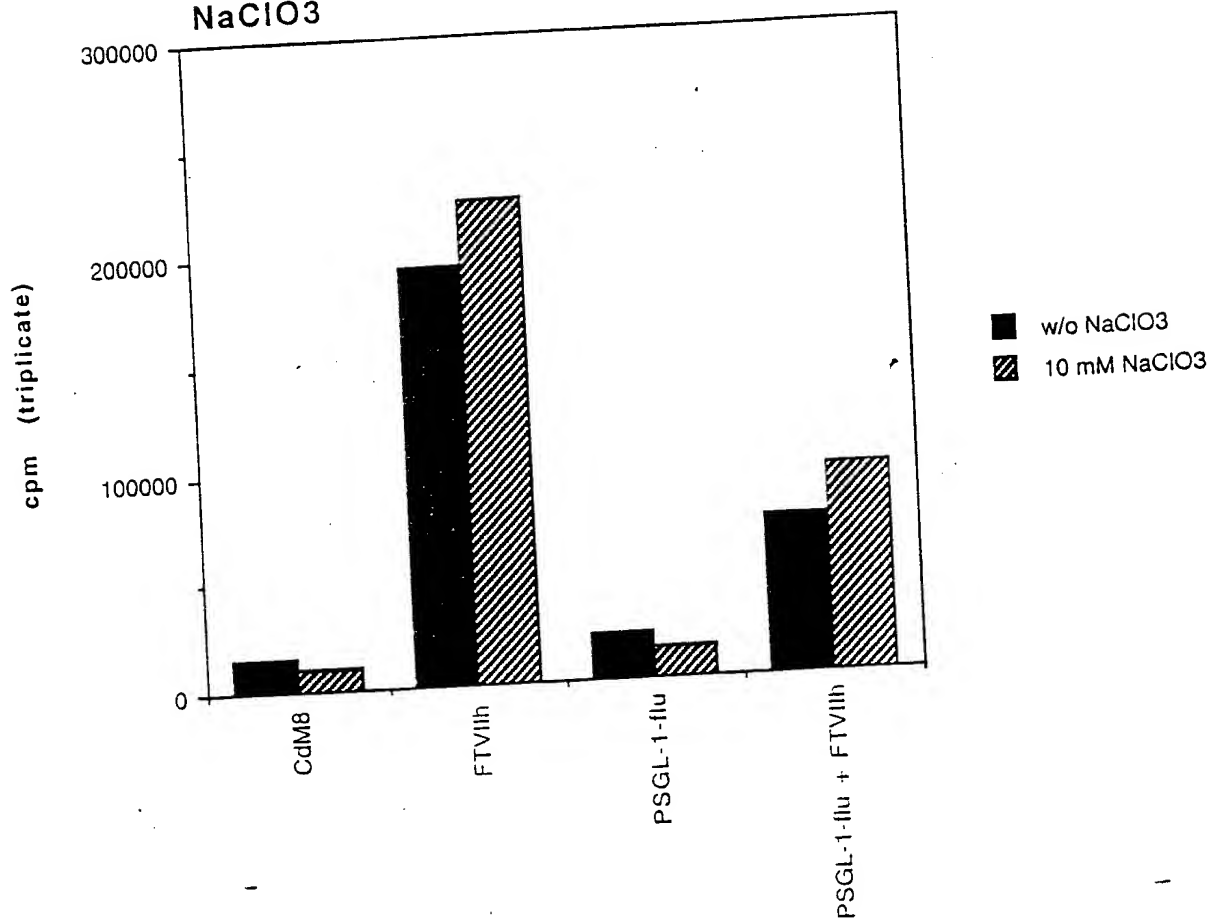


FIG. 7

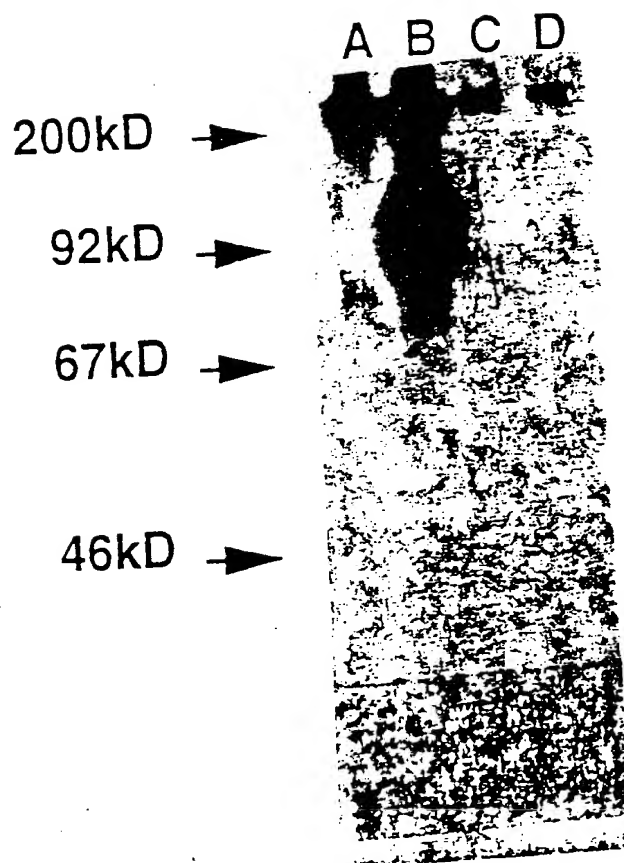
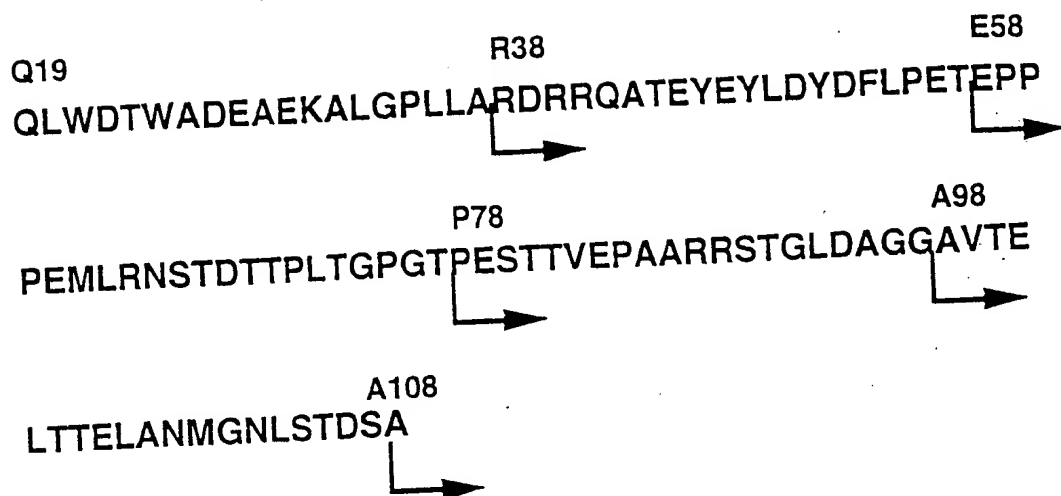


FIG. 8A

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FIG. 8B

P-Selectin Binding to COS M6 Cells
Expressing PSGL-1-NH2 Terminus Deletion
Mutants

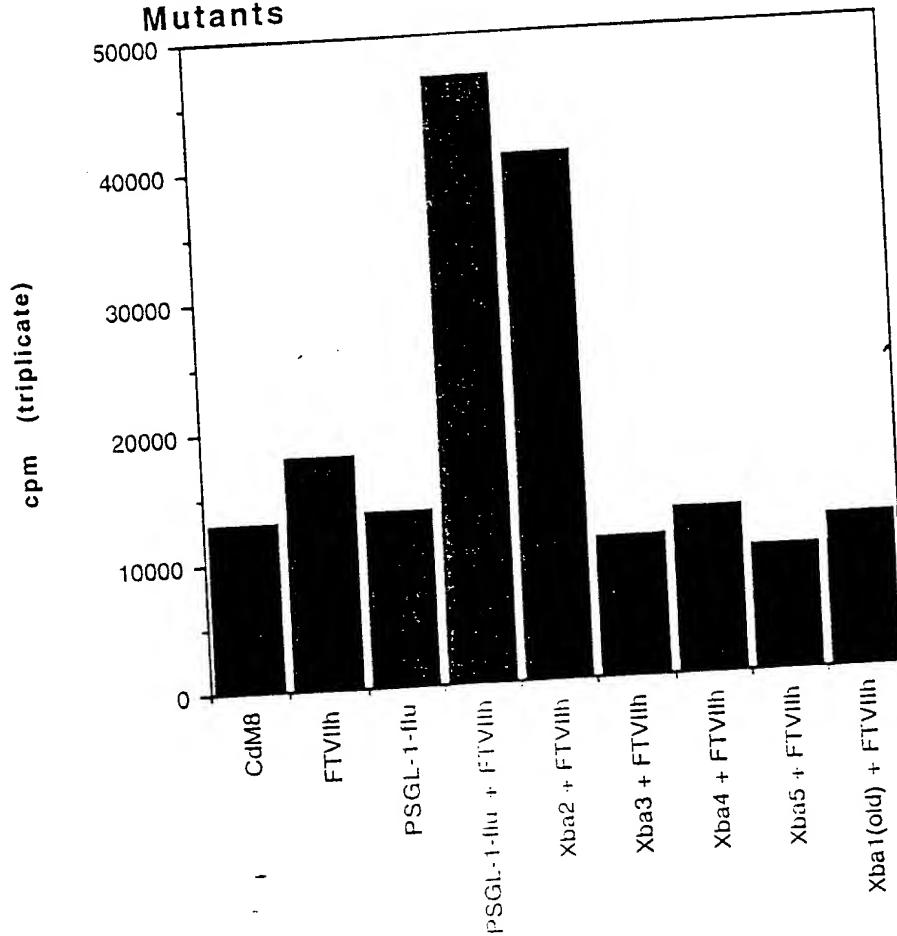
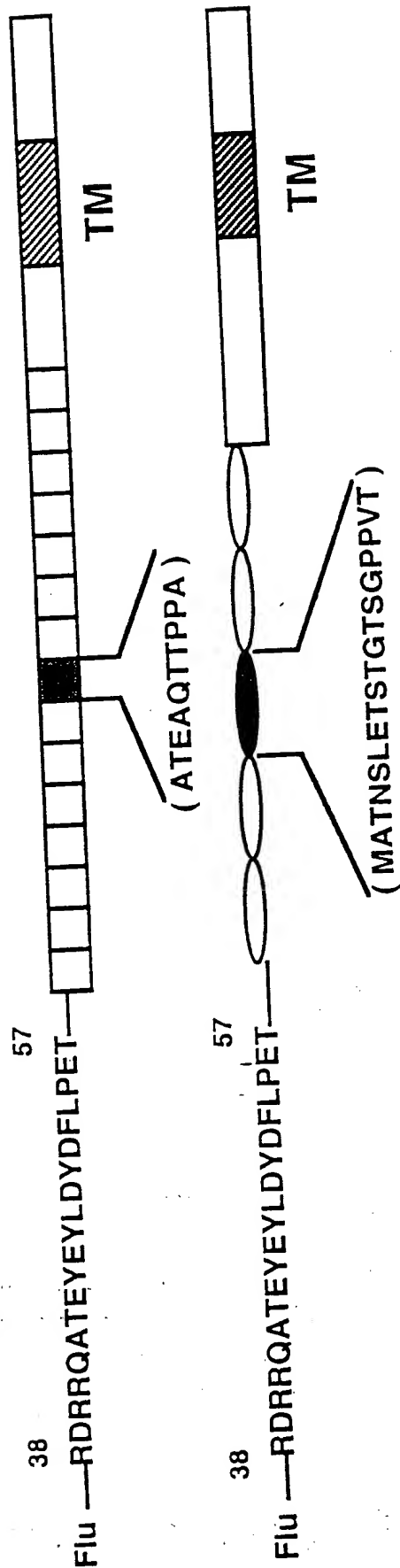


FIG. 9A

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Expression (MFI)

Binding

Construct

4.8
4.5
4.5
5.8
4.3

3.1
3.0
3.7
3.3

++
++
--
--
--

++
--
--
--

1R1
1R1-WT
1R1-Y/F
1R1-T/A
1R1-Y/F/T/A

CD43-WT
CD43-Y/F
CD43-T/A
CD43-Y/F/T/A

FL-PSGL-1
— RRRQATEYDYDFLPET — PSGL-1
— RRRQATEFEFLDFLPEA — PSGL-1
— RRRQAAEYDYDFLPEA — PSGL-1
— RRRQAAEFELDFLPEA — PSGL-1

— RRRQATEYDYDFLPET — CD43
— RRRQATEFEFLDFLPEA — CD43
— RRRQAAEYDYDFLPEA — CD43
— RRRQAAEFELDFLPEA — CD43

P-Selectin Binding to COS M6 Cells
Expressing Wild-Type and Mutant 20 aa
Binding Domain

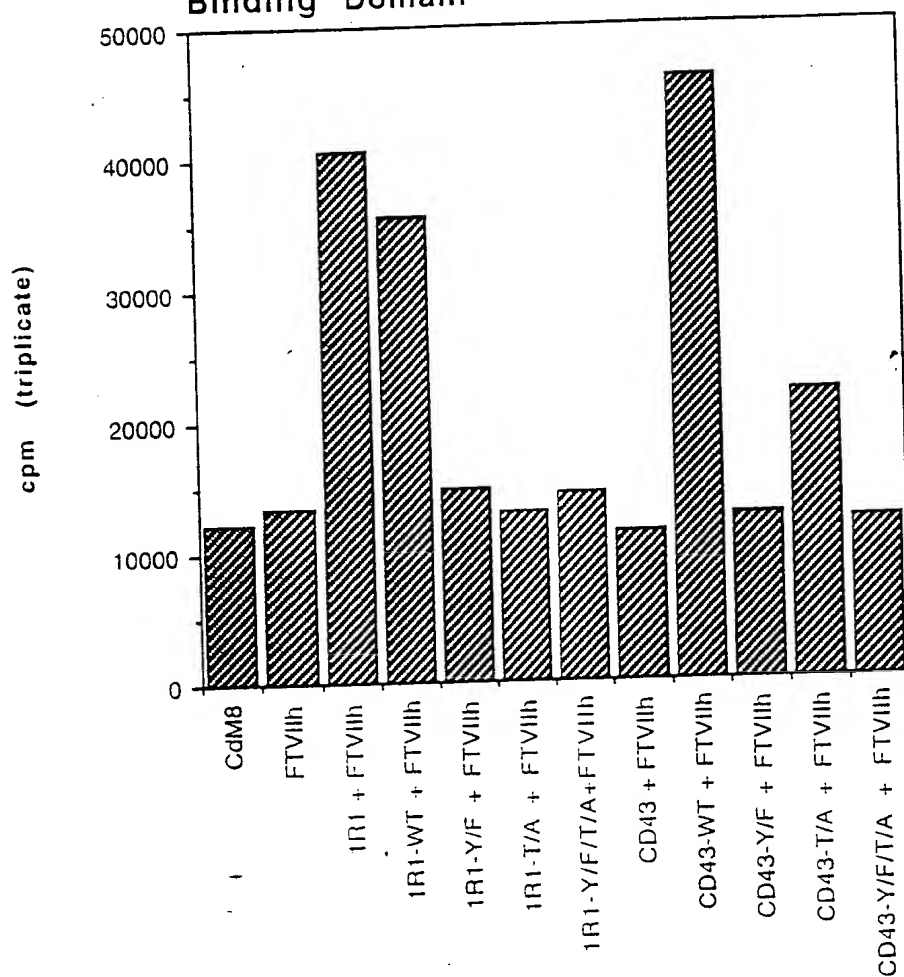


FIG. 10

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AAGCTTACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTTCTGGTGGCAGCAGTTACA
 TTCCGAATGGTGGTACCTTACCTTACCTTCAAGGAGAAGAAACACCACCCTCTCTCATGT 60
 K L T T M L W T W R F L F F V V A A A T -

GTCTTCAGTCCGAGGTTCAGCTCTTCCAGTCTCGGGCTCAGGTCAAGAAGCCTTCTTCC
 TCACAGGTGAGGGTCCAGCTCCACCACGTGAGACCCCGACTCCACTTCTTCCGAGCCAGG 120
 G V Q E Q V Q L V Q S G A E V K K F G E -

TCGGTGAAGGTCTCCTTCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTCC
 AGCCACTTCCAGAGGACCTTCCGAAGACCTCCCTCGAAGTCCCTCGATACGATAGTCCACC 180
 A V K V E C F A S G G T F S S Y A I W -

GTGGCAGAGGCCCTCTGACAAAGGCTTCAAGTGGATCGGAGCGATCATCCCTATCTTTGGT
 CACCGCTCTCCCGGGACCTTTCCCGAACTCACCTACCTCCCTAGTAGGGATAGAAACCA 240
 V R Q A P Q Q L E W M G G I P I F Q -

ACAGCAAACTACGCAATAAATTCCAGGGGAGAGTGCAGCATACCCCGGACGAATCCAGG
 GTCTCTTTGATGCTCTTTTCAAGGTCCCTCTCAGTGCCTAATGCCCGCTCTTTAGTTCC 300
 A H Y A L F V Q Q R V T I T A D E C T -

BH
 CG

F 3S
 H AGE H MD 3SA BD

EXH

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AGCACAGCCTACATGAGGTTAGGAMGTTAGATCTGAGGACACGCGCTTTATTATTCT
 TCGTGTCCGATGTACCTGCAATCTCTGCAATCTAGACTCTCTGCGCTTACATAATATA

GCGAGAGATAATGAGCCTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCCAGCCC
 CGCTCTCTATTACCTCGCATAACATCACCACCATCGACGATGAGCCCCACCAAGCTGGG

A R D N H A Y L D G G S C Y S G W F D P

TGGGGCCAGGGAACCCCTGGTCACCGTCTCTTCAGGTGAGTACTGAAATCTAGCTTTCTCG
 ACCCCCGTCCCTTGGGACCACTGGCAGAGAAGTCCACTCATGACTTAAGATCGAAGACC

W G Q G T L V T V S S

GCGAGGCCAGGCTGACCTTGGCTTTGGGGCAGCGAGCGGGCTAAGGTGAGGCAAGGTGG
 CGGTCCCGTCCGACTGGAACCGAAACCCCTCCCTCCCGCGATTGAGTCCGTCCAGCC

GCCAGCAGGTGCACACCCATGCCCCATGAGCCCCAGACACTGGACCGTGAALLTCCCGGAC
 CGGTCCGTCCACGTGTGGGTTACCGGTACTCCGGTCTGTGACCTCCGACTTCGAGCGCCCTG

AGTTAAGAACCCAGGGGGCTCTGCGCCCTGGGCCCCAGCTCTGTCCGACACCCCGGTGAGAT
 TCAATTCTTGGGTCCCGCGAGACCGCGACCCCGGTCCAGACAGGGTCTGCGCCCGAGTSTA

250220" 8T095280

661 TCCACGACCTCTCTTTTACGCTTCAACAAKAGCCCATCTCTTCTTCCCTTCAACCTTCC
 TCCCTCTCGAGAGAACCTTCCAGCTTCTTCCCTTACCCAGAACGCGGACCTCTTACG

A T K P I V F P L A I

721 TCCAAGAGCACCTCTTGGGGGACAGCGGCCCTGGGCTTCCCTGGTCAAGGACTAGTTTCCC
 AGGTTCTCTCTCGAGACCCCTCTTCCCTGGGACCCGACCGACCACTTCTCTGATGAAGGGG

S K C T D G G T A A C G C L V K D Y F P

781 GAACCCCTGACCGCTCTCTTGGAACTCAGGCGCCCTGACCAAGCGCGCTGCACACCTTTCCC
 CTTGGCCACTGCCACAGCACCTTCTAGTCCCTGGGACTCTCTCCCTGACCTCTCGAAGGGC

E P V T V C W H E G A L T C G V H T F P

841 GCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCCTGCTGACCTTCCCTTCCAGC
 CGACAGGATCTCAGGAGTCTCTGATCAGGGAGTCTCTCCCACTTCCACCGGAGTTCC

A V L Q C C G L F I L C T V T V P I I

901 AGCTTGGGCACCCAGACCTACATCTGCAACCTGAATCACAAGCCCAGCAACACCAAGGTG
 TCGAACCCCTGGGTCTGGATCTAGACCTTCCACTTAGTCTTCCGGTCTCTGCTTCCAC

961 TACAAGAAAGTCTCTGAGAGGCGAGCACAGGGAGGGAGGCTCTCTCTGCAAGCAAGTCTC
 CTGTTCTTTCAACCACTCTCCCTCTCTCTCCCTCCCTCCACAGACCACTTCTTCTGAG

D K K V

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1021 AGCGCTCCTCCCTGGACCCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCAGGC

TCGGCAGGACGGACCTCCCTAGGGCCCATACGTCCGGGTCAGGTCCCGTCGTTCGGTCCG 1080

1081 CCGCTCTGCGCTCTTCACCGGAGCGCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCT

GGGCAGACGGAGAAGTGGCCCTCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGAG 1140

1141 CTGGGCTTTTTCCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCCTAACCCAGGGCCCTGC

AGACCGAAAAAGGGTCCGAGACCCGTCCGTGTCCCATCCACGGGGATTGGGTCCGGGACG 1200

1201 ACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGGAGGACCCCTGC

TGTGTTTCCCCGTCCACGACCCGAGTCTGGACGGTTCTCGGTATAGGCCCTCCTGGGACG 1260

1261 CCCTGACCTAAGCCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCCGACACCTTCT

GGGACTGGATTCCGGTGGGGTTTCCGGTTTGAGAGGTGAGGGAGTCCAGCCCTGTGGAAGA 1320

1321 CTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCGAGAGCCCAAATCTTGTGACAA

GAGGAGGGTCTAAGGTCATTGAGGGTTAGAAGAGAGACGTCTCGGGTTTAGAACACTGTT 1380

E P K S C D K -

1381 AACTCACACATGCCCCACCGTCCCCAGGTAAGCCAGCCCAGGCCCTCGCCCTCCAGCTCAAG

TTGAGTGTGTACGGGTGGCACGGGTCCATTTCGTCCGGTCCGGAGCGGGAGGTCCGAGTTC 1440

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1441 GCGGGACAGGTGCCCTAGAGTAGCCTCCATCCAGGGACAGGCCCCAGCCGGTGCCTACA

CGCCCTGTCCACGGGATCTCATCGGACGTAGGTCCCTGTCCGGGGTCCGCCCCACCACTGT 1500

1501 CGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCT

GCAGGTGGAGGTAGAGAAGGAGTCTCTGCACTTGAGGACCCCCCTGGCAGTCAGAAGGAGA 1560
A P E L L G G P S V F L F -

1561 TCCCCC AAAACCC AAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCCGTGG

AGGGGGGTTTTGGGTTCTCTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACCCACC 1620
P P K P K D T L M I S R T P E V T C V V -

1621 TGGTGGACCTGAGCCACGAGACCCCTCAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG

ACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCCCACC 1680

- V D V S H E D P E V N S
K F N W Y V D G V E -
274 281
(top) (bot)

1681 AGGTGCATAATCCCAAGACAAAGCCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGG

TCCACGTATTACGGTCTCTTTCCGGCGCCCTCCTCTCATGTTCTCGTGCATGGCCCCACC 1740

V H N A K T K P R E E N S
V V V V V X X X / / / Q Y N C T Y R V V -
292 295 297
(top)

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1741 TCAGCGTCCTCACCCTCCTCCACCAGGACTGGCTGAATGCCAAGGAGTACAAGTCCAAGG

AGTCCGAGGAGTGGCAGGACCTCGTCTCTGACCGACTTACCGTTCCTCATGTTACCGTTCC 1800

S V L T V L H Q D W L N G K E Y K C N V -
318 320 322

1801 TCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGTGGGA

AGAGGTTGTTTTCGGGAGGGTCCGGGGTAGCTCTTTTGTAGAGGTTTCGGTTTCCACCCCT 1860

S N K A L P A P I E K T I S K A K
331 333 335 337

1861 CCGGTGGGGTGGCAGGGCCACATGGACAGAGGCCGGCTCGGCCCCACCCCTCTGCCCTGAGA

GGGCACCCACGCTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGGACTCT 1920

1921 GTGACCCCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCC

CACTGGCGACATGGTTGGAGACAGCATGTCCCGTCCGGGGCTCTTGGTGTCCACATGTGGG 1980

G Q P R E P Q V Y T L -

1981 TGCCCCCATCCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCCTGGTCAAAG

ACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCCGACTGGACGGACCAGTTTC 2040

P P S R D E L T K N Q V C L T C L V K G -

2041 GCTTCTATCCCAGCGACATCGCCCTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC

2100

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CGAAGATAGGGTCCCTGTAGCGGCACCTCACCCTCTCTTACCCCTCGGGCTCTCTCA

F Y P S D I A V E W E S H G Q P E H H Y -

2101 ACAAGACCACGGCTCCCTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCA 2160
TGTTCTCGTGCCGAGGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCCTTCGAGT

K T T P P V L D S D G S F F L Y S K L T -

2161 CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG 2220
GGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACCTACGTACTCC

V D K S R W Q Q G N V F S C, S V M H E A -

2221 CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGAGTCCGAC 2280
GAGACGTGTTGGTGATGTCCGTCTTCTCGGAGAGGGACAGAGGCCCATTTACTCAGGCTG

L H N H Y T Q K S L S L S P G K .

2281 GGCCGGC
CCGGCCG

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1 ATGGCGCTGT CCTGGGTTCT TACAGTCCTG AGCCTCCTAC CTCTGCTGGA
51 AGCCCAGATC CCATTGTGTG CCAACCTAGT ACCGGTGCCC ATCACCAACG
101 CCACCCTGGA CCAGATCACT GGCAAGTGGT TTTATATCGC ATCGGCCTTT
151 CGAAACGAGG AGTACAATAA GTCGGTTCAG GAGATCCAAG .CAACCTTCTT
201 TTA CTTCACC CCCAACAAGA CAGAGGACAC GATCTTTCTC AGAGAGTACC
251 AGACCCGACA GGACCAGTGC ATCTATAACA CCACCTACCT GAATGTCCAG
301 CGGGAAAATG GGACCATCTC CAGATACGTG GGAGGCCAAG AGCATTTCGC
351 TCACTTGCTG ATCCTCAGGG ACACCAAGAC CTACATGCTT GCTTTTGACG
401 TGAACGATGA GAAGAACTGG GGGCTGTCTG TCTATGCTGA CAAGCCAGAG
451 ACGACCAAGG AGCAACTGGG AGAGTTCTAC GAAGCTCTCG ACTGCTTGCG
501 CATTCCCAAG TCAGATGTCTG TGTACACCGA TTGGAAAAAG GATAAGTGTG
551 AGCCACTGGA GAAGCAGCAC GAGAAGGAGA GGAAACAGGA GGAGGGGGAA
601 TCGGATCCCC AGGGTGAGTA CTAAGCTTCA GCGCTCCTGC CTGGACGCAT
651 CCCGGCTATG CAGCCCCAGT CCAGGGCAGC AAGGCAGGCC CCGTCTGCCT
701 CTTCA CCCGG AGCCTCTGCC CGCCCCACTC ATGCTCAGGG AGAGGGTCTT
751 CTGGCTTTTT CCCAGGCTCT GGGCAGGCAC AGGCTAGGTG CCCCTAACCC
801 AGGCCCTGCA CACAAAGGGG CAGGTGCTGG GCTCAGACCT GCCAAGAGCC
851 ATATCCGGGA GGACCCTGCC CCTGACCTAA GCCCACCCA AAGGCCAAAC
901 TCTCCACTCC CTCAGCTCGG ACACCTTCTC TCCTCCCAGA TTCCAGTAAC
951 TCCCAATCTT CTCTCTGCAG AGCCCAAATC TTGTGACAAA ACTCACACAT
1001 GCCCACC GTG CCCAGGTAAG CCAGCCCAGG CCTCGCCCTC CAGCTCAAGG
1051 CGGGACAGGT GCCCTAGAGT AGCCTGCATC CAGGGACAGG CCCCAGCCGG
1101 GTGCTGACAC GTCCACCTCC ATCTCTTCCT CAGCACCTGA ACTCCTGGGG
1151 GGACCGTCAG TCTTCCTCTT CCCCCCAAAA CCCAAGGACA CCCTCATGAT

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1201 CTCCCGGACC GAGGTCA CATGCGTGGT GGTGCTG AGCCACGAAG
1251 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGGA GGTGCATAAT
1301 GCCAAGACAA AGCCGCGGGA GGAGCAGTAC AACAGCACGT ACCGGGTGGT
1351 CAGCGTCCTC ACCGTCCTGC ACCAGGACTG GCTGAATGGC AAGGAGTACA
1401 AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA GAAAACCATC
1451 TCCAAAGCCA AAGGTGGGAC CCGTGGGGTG CGAGGGCCAC ATGGACAGAG
1501 GCCGGCTCGG CCCACCCTCT GCCCTGAGAG TGACCGCTGT ACCAACCTCT
1551 GTCCTACAGG GCAGCCCCGA GAACCACAGG TGTACACCCT GCCCCCATCC
1601 CGGGATGAGC TGACCAAGAA CCAGGTCAGC CTGACCTGCC TGGTCAAAGG
1651 CTTCTATCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT GGGCAGCCGG
1701 AGAACAACTA CAAGACCACG CCTCCCGTGC TGGACTCCGA CGGCTCCTTC
1751 TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC AGCAGGGGAA
1801 CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC CACTACACGC
1851 AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GAGTGCGACG GCCG

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1 MALSWVLTVL SLLPLLEAQI PLCANLVPVP ITNATLDQIT GKWFYIASAF
51 RNEEYNKSVQ EIQATFFYFT PNKTEDTIFL REYQTRQDQC IYNTTYLNVQ
101 RENG TISRYV GGQEHFAHLL ILRDTKTYML AFDVNDEKNW GLSVYADKPE
151 TTKEQLGEFY EALDCLRIPK SDVVYTDWKK DKCEPLEKQH EKERKQEEGE
201 SDPEGEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT
251 CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH
301 QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK
351 NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL
401 TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK*

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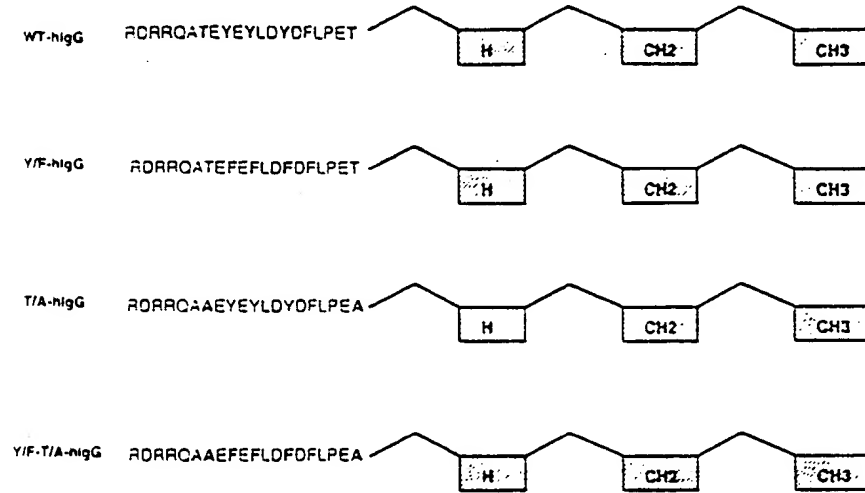
Constructs

FIG. 12A

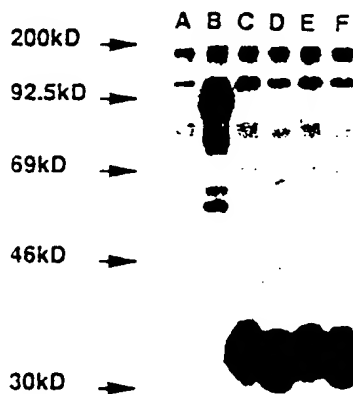


FIG. 12B

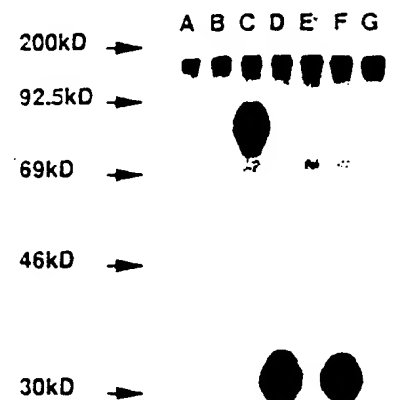


FIG. 12C

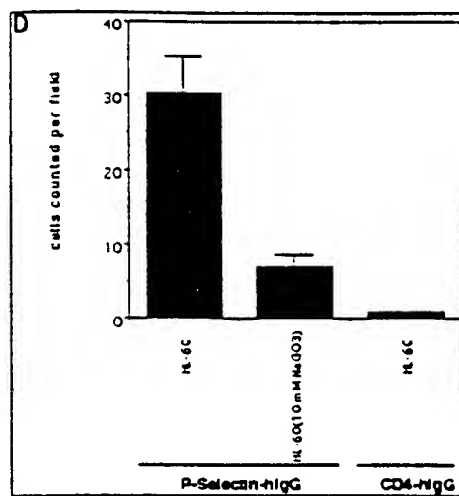


FIG. 13

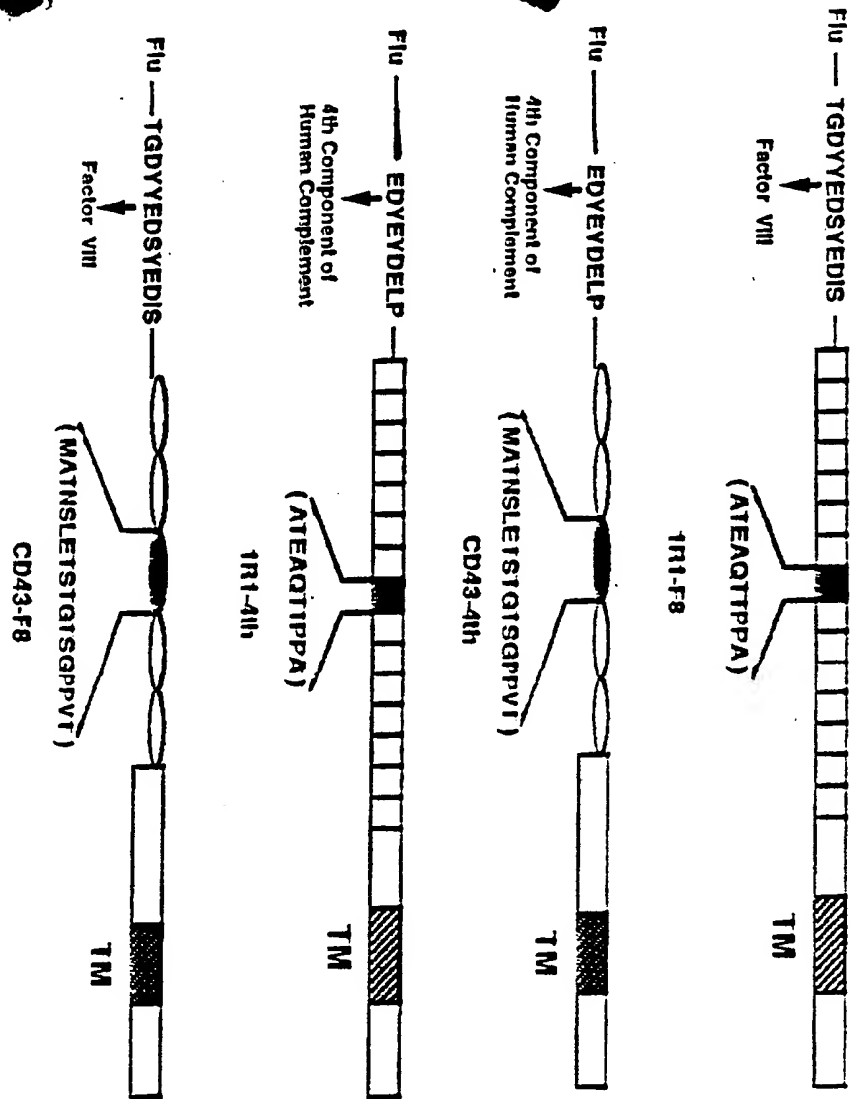


FIG. 14

**P-Selectin Binding to COS M6 Cells
Expressing Artificial Chimeric Proteins**

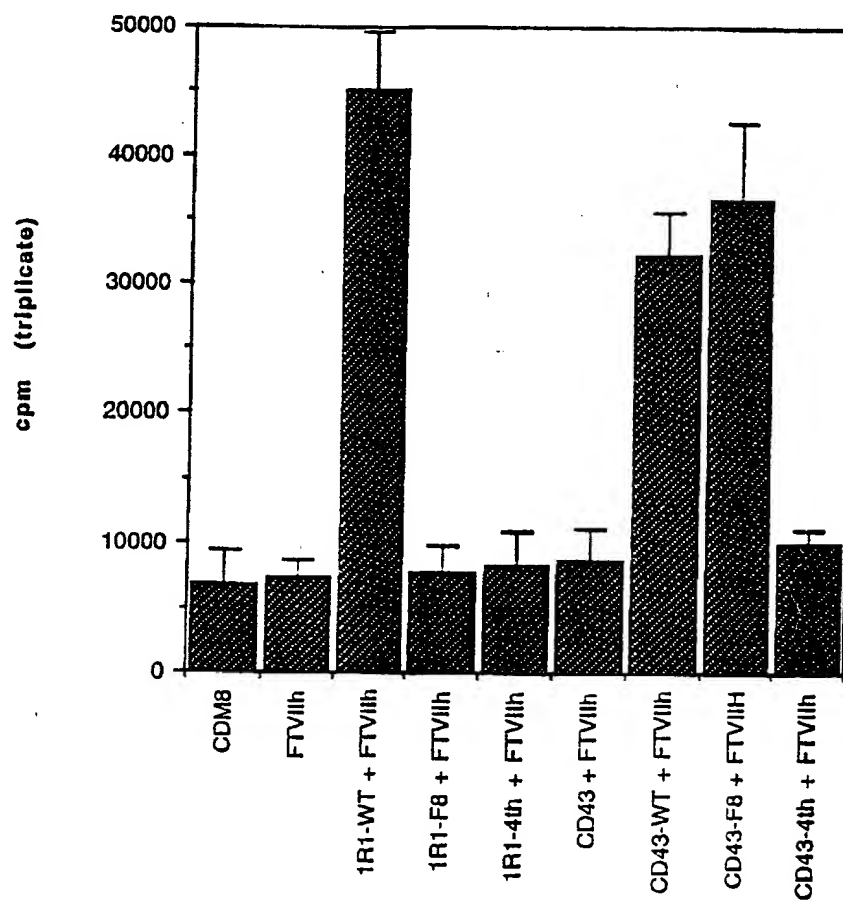


FIG. 15